

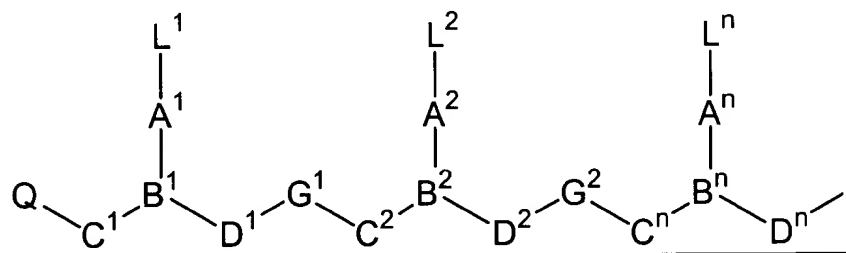
(iii) *Amendment To The Claims:*

1. (Currently Amended) A ~~non-nucleic acid~~ PNA probe of 10 to 30 subunits in length ~~having~~ comprising a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-

ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41);
 GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-
 TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-
 TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA
 (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-
 AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID
 No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-
 GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No.
 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-
 TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124);
 GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-
 AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127);
 ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-
 AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50);
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 CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-
 TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq.
 ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-
 GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No.
 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-
 TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-
 AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT
 (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); CAG-TTC-
 ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID
 No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-
 ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134);
 ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-
 GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-
 CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq.
 ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-
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ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA-E (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG-E (Seq. ID No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID

No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159) wherein said PNA probe has the formula:



wherein,

n is at least 2,

each of L¹-Lⁿ is independently selected from the group consisting of hydrogen, hydroxy, (C₁-C₄)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C¹-Cⁿ is (CR⁶R⁷)_y where R⁶ is hydrogen and R⁷ is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R⁶ and R⁷ are independently selected from the group consisting of hydrogen, (C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is

hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z, where R⁶ and R⁷ are as defined above;

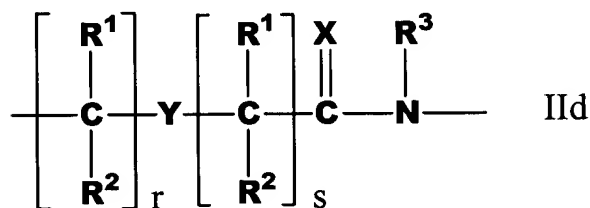
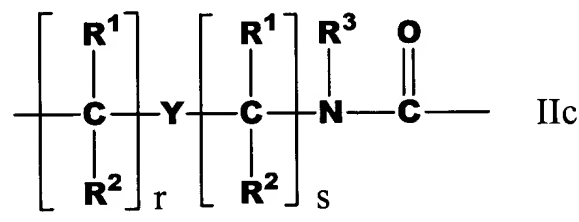
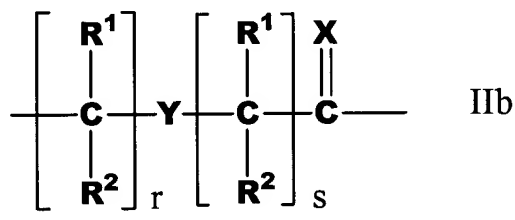
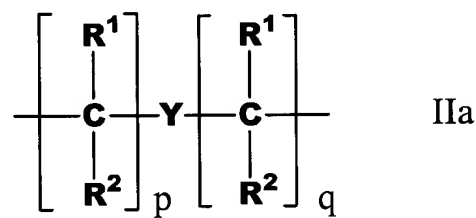
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R³N⁺; or

(b) A is a group of formula (IIId) and B is CH₃;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

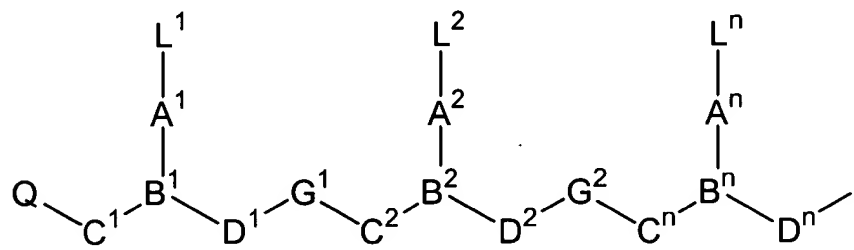
Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

2. (Original) The probe of claim 1, wherein the probing nucleobase sequence is exactly as represented in the claim.
3. (Original) The probe of claim 1, wherein the probing nucleobase sequence is 16-23 subunits in length.
4. (Original) The probe of claim 1, wherein the probe is unlabeled.
5. (Original) The probe of claim 1, wherein the probe is labeled with at least one detectable moiety.
6. (Original) The probe of claim 5, wherein the detectable moiety or moieties are selected from the group consisting of: a dextran conjugate, a branched nucleic

acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.

7. (Original) The probe of claim 1, wherein the probe is labeled with at least two independently detectable moieties.
8. (Original) The probe of claim 7, wherein the two or more independently detectable moieties are independently detectable fluorophores.
9. (Original) The probe of claim 1, wherein the probe is support bound.
10. (Currently Amended) A probe set comprising at least thirteen ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length and that is suitable for detecting, identifying or enumerating human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and/or 20, as well as 13/21 as a pair, in a sample wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen,

(C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z, where R⁶ and R⁷ are as defined above;

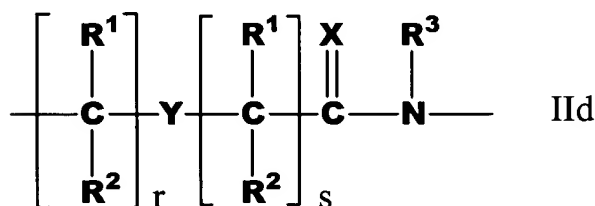
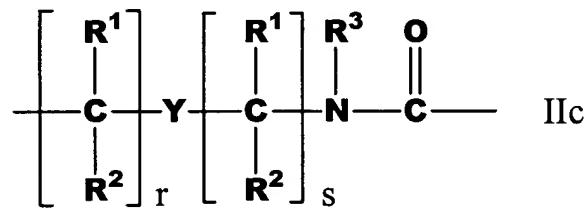
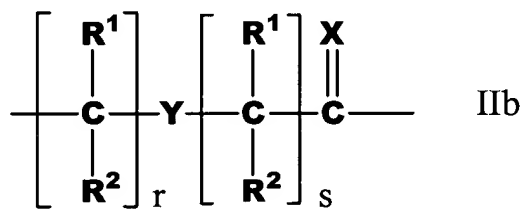
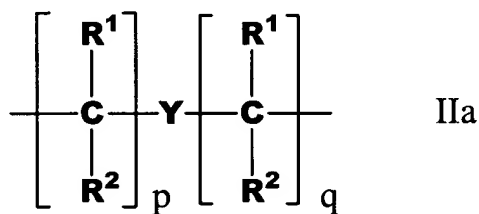
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (II d), and B is N or R³N⁺; or

(b) A is a group of formula (II d) and B is CH;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

11. (Currently Amended) The probe set of claim 10, wherein:

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome X ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-

TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8) and TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome Y ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15) and GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 1 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17) and CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 2 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT

(Seq. ID No. 25) and TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 3 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); and AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 4 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-
 ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-
 AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No.
 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-
 TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-
 AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No.
 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-
 AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); and CTC-ATA-AAA-
 ACC-AGA-AAG-AG (Seq. ID No. 129);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for
 detecting human chromosome 6 ~~have~~ comprise a probing nucleobase
 sequence, at least a portion of which is at least ninety percent homologous
 to the nucleobase sequences, or their complements, selected from the group
 consisting of:

CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-
 AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C
 (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53);
 GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-
 TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT
 (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57);
 GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-
 GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT
 (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61);
 CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-
 TGC-ACA-CAT (Seq. ID No. 63) and TAC-CAA-GAG-GAA-TGT-TGC
 (Seq. ID No. 64);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for
 detecting human chromosome 7 ~~have~~ comprise a probing nucleobase
 sequence, at least a portion of which is at least ninety percent homologous
 to the nucleobase sequences, or their complements, selected from the group
 consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 8 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69) and CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 9 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATG-ATG-AAA-AAG-GTA-ATA-E (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG-E (Seq. ID No. 146);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 10 ~~have~~ comprise a probing nucleobase

sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76) and GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 11 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82) and GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 12 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-

TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95) and CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 16 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100) and AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 17 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110) and AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 18 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 20 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

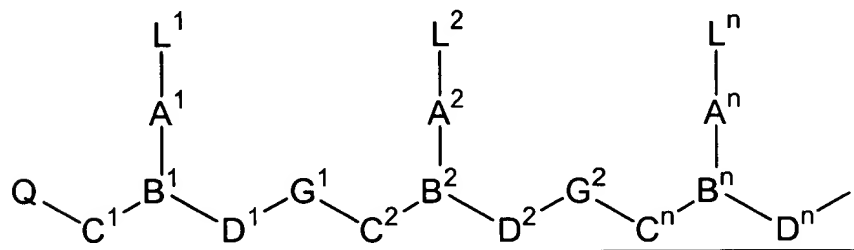
ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152);

the one or more ~~non-nucleic acid~~ PNA probes of the set specific for detecting human chromosome 13/21 ~~have~~ comprise a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159).

12. (Original) The probe set of claim 11, wherein the probing nucleobase sequence of the probes of the set are exactly as represented in the claim.

13. (Original) The probe set of claim 11, wherein two or more probes of the set are independently detectable.
14. (Original) The probe set of claim 13, wherein one or more of the independently detectable probes are labeled with two or more independently detectable moieties.
15. (Original) The probe set of claims 13, wherein the independently detectable probes are used to distinguish between human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and 20, as well as 13/21 as a pair.
16. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 4 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:
- ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128) and CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129)
- wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L¹-Lⁿ is independently selected from the group consisting of hydrogen, hydroxy, (C₁-C₄)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C¹-Cⁿ is (CR⁶R⁷)_y where R⁶ is hydrogen and R⁷ is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R⁶ and R⁷ are independently selected from the group consisting of hydrogen, (C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z where R⁶ and R⁷ are as defined above;

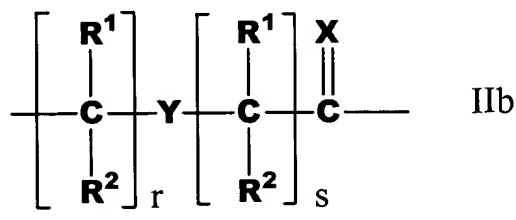
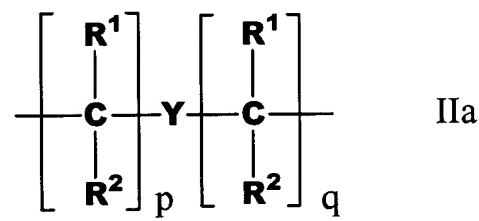
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

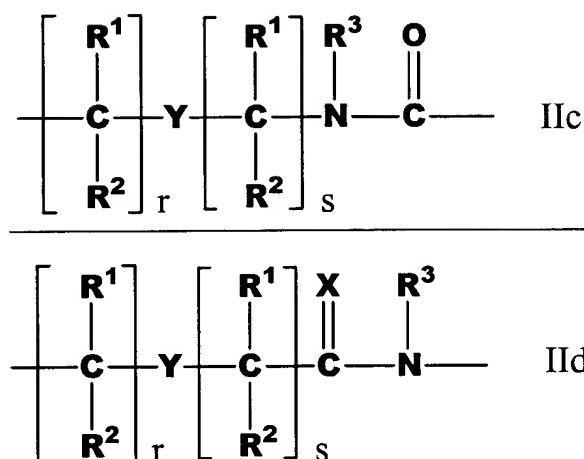
each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R³N⁺; or

(b) A is a group of formula (IId) and B is CH;





where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

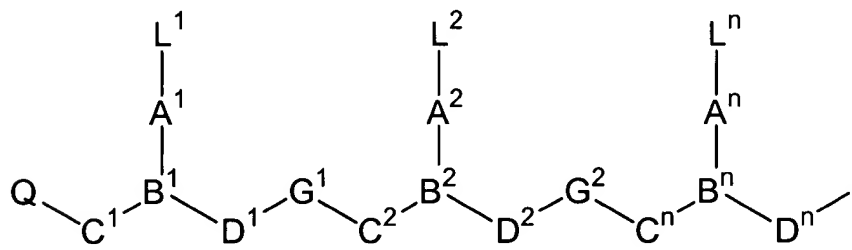
Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

17. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or

number of human chromosome 7 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$, where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, $(C_1$ -

C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z where R⁶ and R⁷ are as defined above;

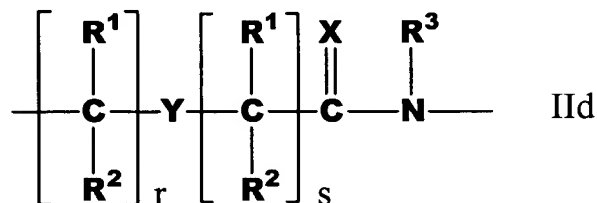
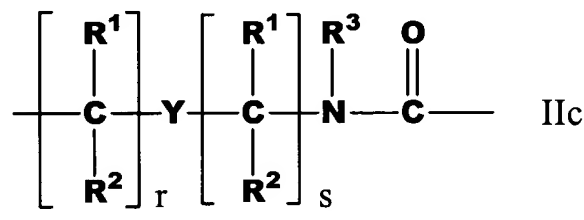
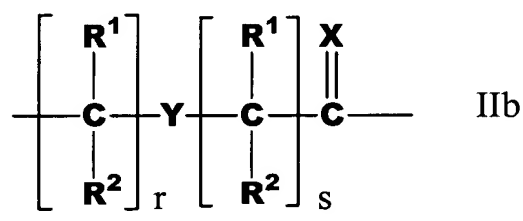
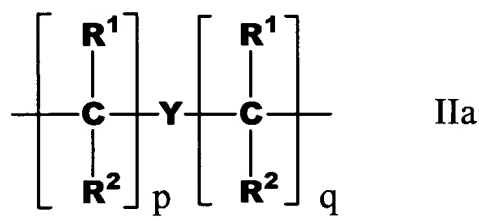
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R³N⁺; or

(b) A is a group of formula (IIId) and B is CH₃;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

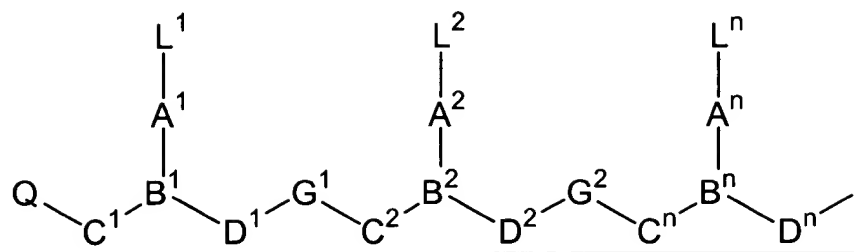
each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

18. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 9 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATG-ATG-AAA-AAG-GTA-ATA-E (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG-E (Seq. ID No. 146) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

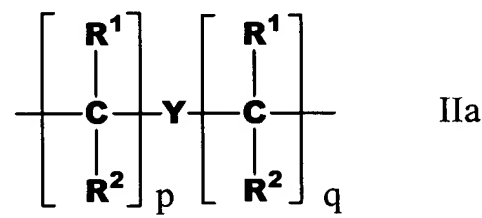
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

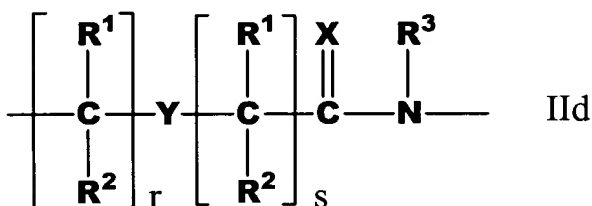
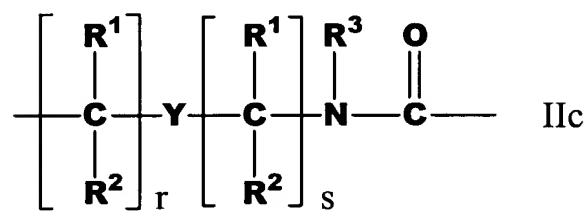
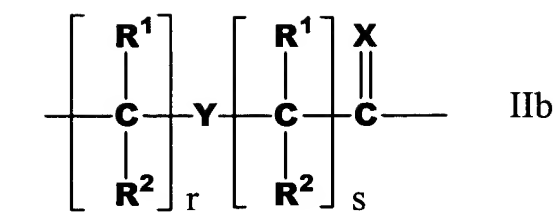
each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or

(b) A is a group of formula (IId) and B is CH;





where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

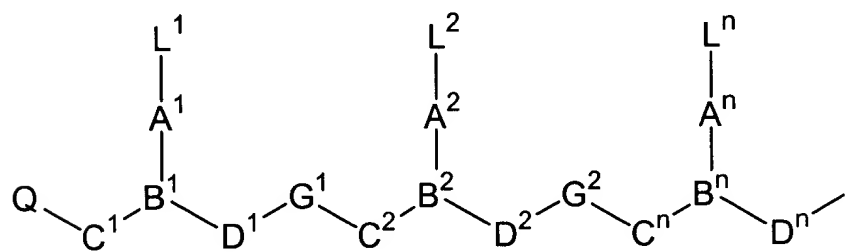
Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl,

amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

19. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosome 20 in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152) wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L¹-Lⁿ is independently selected from the group consisting of hydrogen, hydroxy, (C₁-C₄)alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C¹-Cⁿ is (CR⁶R⁷)_y where R⁶ is hydrogen and R⁷ is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R⁶ and R⁷ are independently selected from the group consisting of hydrogen, (C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-

C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z where R⁶ and R⁷ are as defined above;

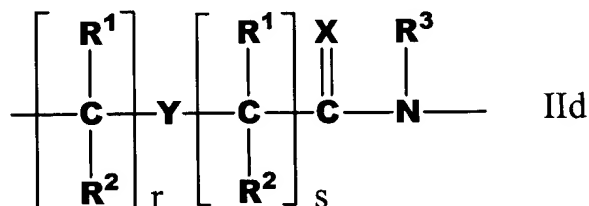
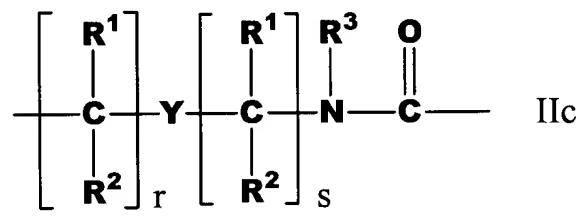
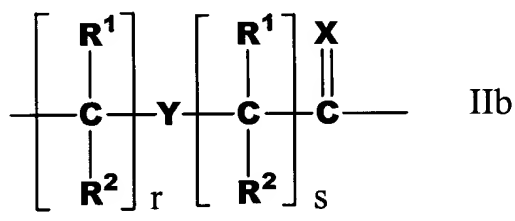
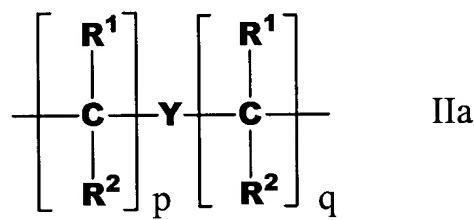
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IIId), and B is N or R³N⁺; or

(b) A is a group of formula (IIId) and B is CH₃;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

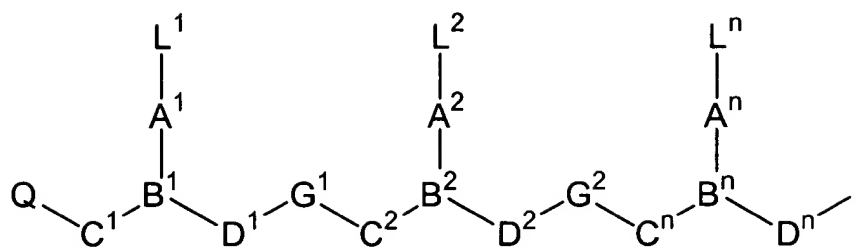
each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

20. (Currently Amended) A probe set comprising ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length suitable for detecting the presence, absence or number of human chromosomes 13 and 21 as a pair in a sample wherein the probing nucleobase sequence of at least one probe comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159)
wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

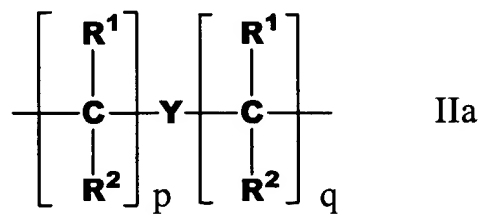
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

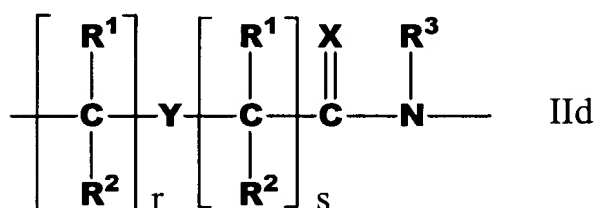
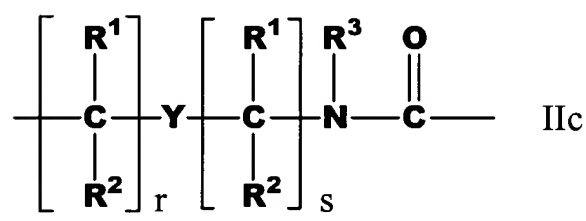
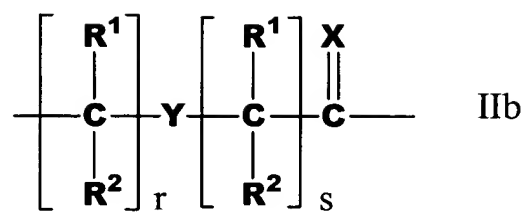
each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or

(b) A is a group of formula (IId) and B is CH;





where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

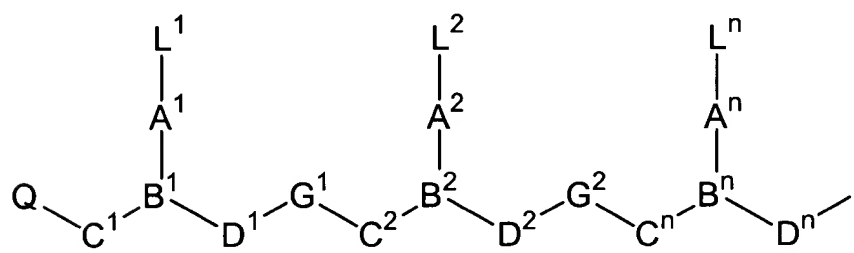
Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl,

amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

21. (Currently Amended) A method for detecting, identifying or quantitating one or more of human chromosomes Y, 1, 2, 3, 4, 7, 6, 9, 8, 10, 11, 12, 16, 17, 18 or 20, as well as chromosomes 13 and 21 as a pair, in a sample, said method comprising:

- a-) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length ~~having~~ comprising a probing nucleobase sequence which is specific for one or more of human chromosomes Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 or 20, as well as 13/21 as a pair; and
- b-) detecting, identify or quantitating hybridization of the probing nucleobase sequence of ~~non-nucleic acid~~ the PNA probe or probes to the target sequences of the chromosomes, and correlating the result with the presence, absence or number of the chromosomes in the sample wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_x$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is

hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z where R⁶ and R⁷ are as defined above;

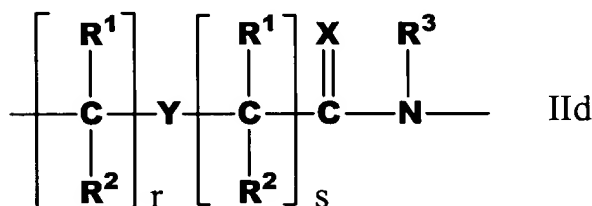
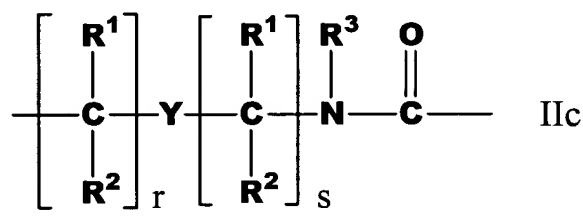
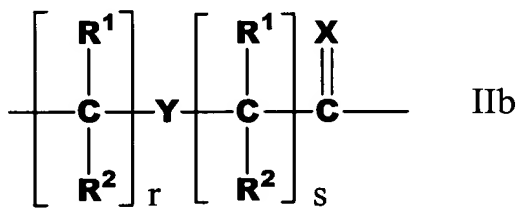
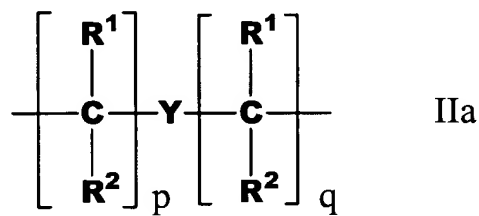
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R³N⁺; or

(b) A is a group of formula (IId) and B is CH;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

22. (Original) The method of claim 21, wherein the probing nucleobase sequence of at least one probe of the set comprises a segment, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq.

ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-
 AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-
 ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT
 (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26);
 ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-
 TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC
 (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No.
 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-
 ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT
 (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34);
 TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-
 ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC
 (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38);
 AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-
 AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-
 CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No.
 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-
 CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC
 (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46);
 TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-
 CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC
 (Seq. ID No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119);
 CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-
 ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-
 TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No.
 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-
 TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-
 AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID
 No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-
 ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-
 GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA

(Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAATTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); CAG-TTC-ATATGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACGGGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA-~~E~~ (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG-~~E~~ (Seq. ID No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-

AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117) and

CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159).

23. (Currently Amended) A method for detecting, identifying or quantitating one or more of human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 or 20, as well as 13/21 as a pair, in a sample, said method comprising:

- a.) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length ~~having~~ comprising a probing nucleobase sequence at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14);

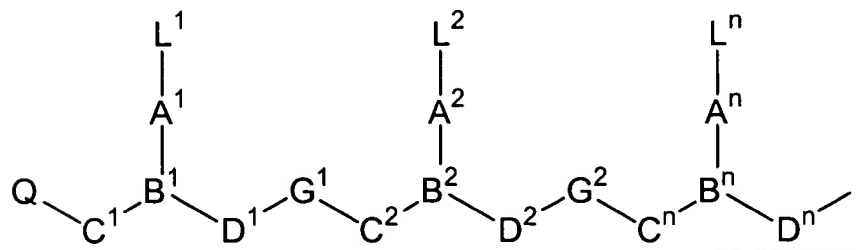
CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-
 CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT
 (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18);
 GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-
 TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT
 (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22);
 GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-
 AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-
 AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC
 (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27);
 GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-
 AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-
 AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No.
 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-
 AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-
 GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID
 No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-
 TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-
 AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq.
 ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40);
 CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-
 AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA
 (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44);
 GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-
 GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG
 (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48);
 AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-
 TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT
 (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No.
 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-
 CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-

AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-

AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-
 ATA-~~E~~ (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG-~~E~~ (Seq. ID
 No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-
 TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-
 ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC
 (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75);
 AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-
 GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC
 (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79);
 CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-
 GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A
 (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83);
 TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-
 GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-
 GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID
 No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-
 CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-
 AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID
 No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-
 TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-
 AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT
 (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96);
 GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-
 CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA
 (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100);
 AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-
 GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT
 (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104);
 TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-
 ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA
 (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108);

ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159); and

- b.) detecting, identify or quantitating hybridization of the probing nucleobase sequence of ~~non-nucleic acid~~ the PNA probe or probes to the target sequences of the chromosomes, and correlating the result with the presence, absence or number of the chromosomes in the sample wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L^1-L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1-C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

each of D^1-D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

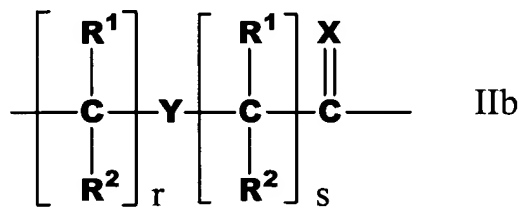
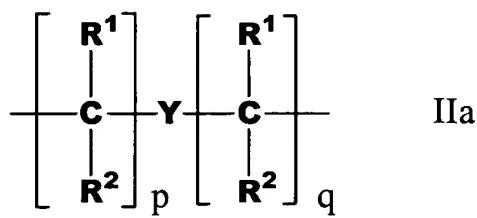
each of y and z is zero or an integer from 1 to 10, the sum $y+z$ being greater than 2 but not more than 10;

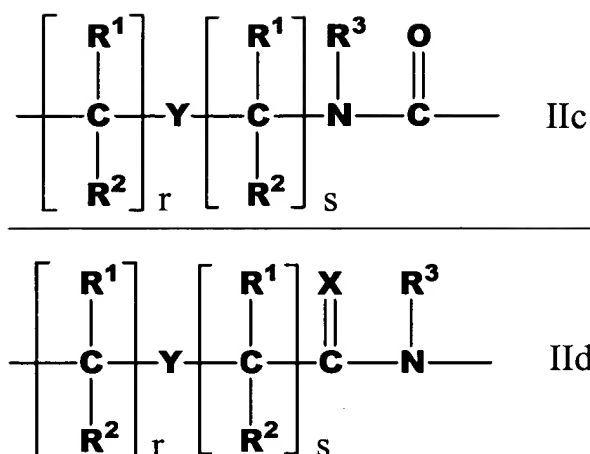
each of G^1-G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1-A^n and B^1-B^n are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or

(b) A is a group of formula (IId) and B is CH_3 ;





where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

24. (Currently Amended) The method of claim 23, wherein the presence, absence or number of human chromosome 4 is determined by:

- a-) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128) and CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); and

- b-) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human X chromosomes in the sample.

25. (Currently Amended) The method of claim 23, wherein the presence, absence or number of human chromosome 7 is determined by:

- a-) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-

GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); and CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); and

- b.) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human Y chromosomes in the sample.

26. (Currently Amended) The method of claim 23, wherein the presence, absence or number of human chromosome 9 is determined by:

- a.) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ATG-ATG-AAA-AAG-GTA-ATA-E (Seq. ID No. 145) and CAT-TCT-CAG-AAC-TGT-TTG-E (Seq. ID No. 146); and

- b.) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 1 in the sample.

27. (Currently Amended) The method of claim 23, wherein the presence, absence or number of human chromosome 20 is determined by:

- a.) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length, wherein at least one probe comprises ~~has~~ a probing nucleobase sequence, at least a portion of which is at least ninety

percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); and GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); and

- b.) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 2 in the sample.

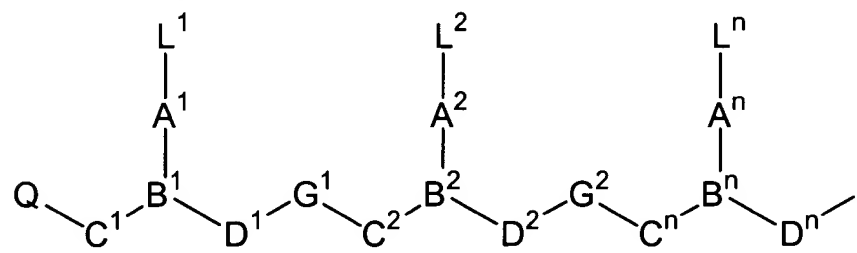
28. (Currently Amended) The method of claim 23, wherein the presence, absence or number of human chromosomes 13 and 21 as a pair is determined by:

- a.) contacting the sample with one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length, wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of:

CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158) and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159); and

- b.) detecting, identifying or quantitating hybridization of the probing nucleobase sequence of the probe or probes to a target sequence in the sample to thereby correlate the result with the presence, absence or number of human chromosome 3 in the sample.

29. (Original) The method of claim 23, wherein *in-situ* hybridization is used to detect, identify or enumerate human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 and 20, as well as 13/21 as a pair, in the sample.
30. (Original) The method of claim 23, wherein the method is used to detect or identify chromosome related abnormalities.
31. (Original) The method of claim 23, wherein the method is used to detect abnormalities in cells, tissues (including bone marrow), spermatozoa, ova, blastomeres, oocysts, buccal cells and chorionic villi.
32. (Original) The method of claim 31, wherein the chromosome related abnormality is aneuploidy or polyploidy.
33. (Original) The method of claim 31, wherein the method is used in preimplantation diagnosis or in prenatal screening.
34. (Currently Amended) A set of ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length for the simultaneous and specific detection of two or more chromosomes wherein the two or more of the probes of the set hybridize to all of the two or more specific chromosomes sought to be detected wherein said PNA probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic

moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C¹-Cⁿ is (CR⁶R⁷)_y, where R⁶ is hydrogen and R⁷ is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R⁶ and R⁷ are independently selected from the group consisting of hydrogen, (C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z, where R⁶ and R⁷ are as defined above;

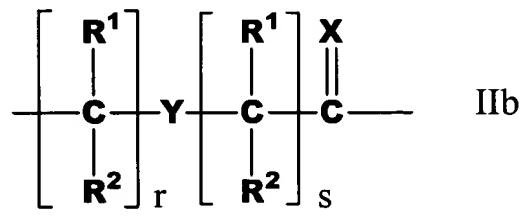
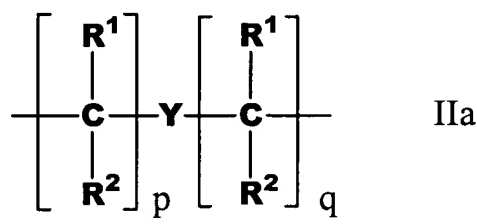
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

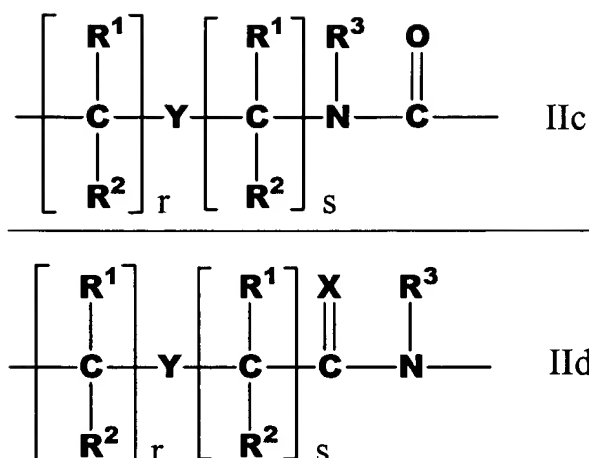
each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R³N⁺; or

(b) A is a group of formula (IId) and B is CH;





where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

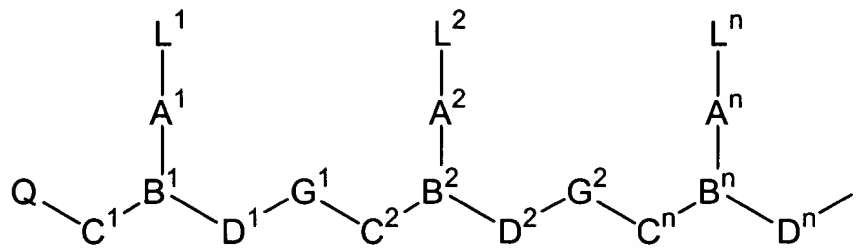
each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

35. (Currently Amended) A set of ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length for the detection, identification or enumeration of human

chromosomes X, Y, 18 and 13/21 as a pair wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

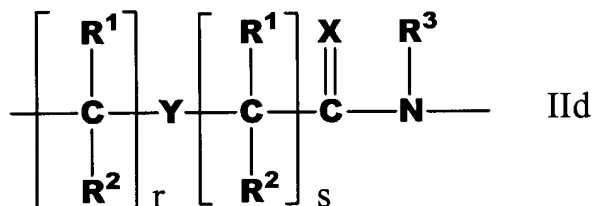
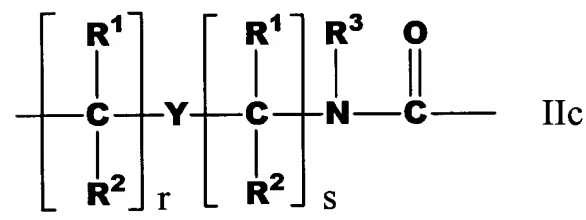
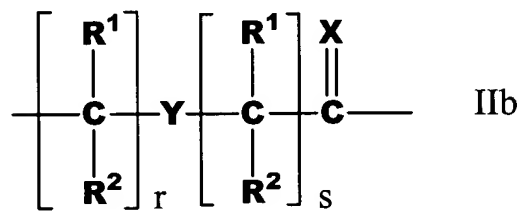
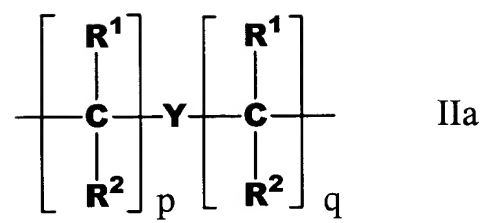
each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or
- (b) A is a group of formula (IId) and B is CH_2 ;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is $-\text{CO}_2\text{H}$, $-\text{CONR}'\text{R}''$, $-\text{SO}_3\text{H}$ or $-\text{SO}_2\text{NR}'\text{R}''$ or an activated derivative of $-\text{CO}_2\text{H}$ or $-\text{SO}_3\text{H}$; and

I is $-\text{NHR}'''\text{R}''''$ or $-\text{NR}'''\text{C}(\text{O})\text{R}''''$, where R' , R'' , R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

36. (Currently Amended) A kit suitable for performing an assay which detects the presence, absence or number of human chromosomes X, Y, 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 16, 17, 18 or 20, as well as 13/21 as a pair, in a sample, wherein said kit comprises:

- a.) one or more ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length wherein at least one probe ~~has~~ comprises a probing nucleobase sequence, at least a portion of which is at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID

No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No. 32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No. 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38); AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41); GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-AAT-CAT-TCG-CAG (Seq. ID No. 48); AGT-GTT-AGA-AAA-CTG-CTC (Seq. ID No. 49); ACA-CGA-TTT-TGG-AAA-CAC (Seq. ID No. 119); CGA-AAC-ATC-ACT-GAG-AGT (Seq. ID No. 120); GGA-TGA-CAT-ATA-ATA-ACT-AG (Seq. ID No. 121); GAA-TTG-AAC-ATT-CAC-TTT-GA (Seq. ID No. 122); TAG-CTC-TGA-AGA-TTT-CGT (Seq. ID No. 123); GAG-ATG-TTT-CCG-AGA-ATG (Seq. ID No. 124); GTG-TAT-TCA-ACT-ACC-AGA (Seq. ID No. 125); ACA-TTT-CTG-TTA-CAG-AGC (Seq. ID No. 126); ATG-ACG-TAT-AAA-ATC-TAG-AG (Seq. ID No. 127); ACG-AAC-ACA-GTT-GAA-CCT (Seq. ID No. 128); CTC-ATA-AAA-ACC-AGA-AAG-AG (Seq. ID No. 129); CTG-TTC-AGA-GTA-ACA-TGA (Seq. ID No. 50); CCG-CTT-GGA-AAT-ACT-ACA (Seq. ID No. 51); GAA-ATG-GAA-ATA-TCT-CCC-C (Seq. ID No. 52); TCT-AGG-AGG-TCC-AAT-TAT (Seq. ID No. 53); GAA-TTC-CCA-AGT-GGA-TAT (Seq. ID No. 54); CTG-TAG-GTT-TAG-ATG-AAG (Seq. ID No. 55); AAG-GAG-TGT-TTC-CCA-ACT (Seq. ID No. 56); GGC-TTC-AAG-GCG-

CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-AGG-GAA-TGT-TCC-ATT (Seq. ID No. 60); CAC-ATA-GCA-GTG-TTT-GAG (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-AAA-TGC-ACA-CAT (Seq. ID No. 63); TAC-CAA-GAG-GAA-TGT-TGC (Seq. ID No. 64); CAG-TTC-ATA-TGT-GCA-GTG (Seq. ID No. 130); GGA-ATA-TCG-TCA-CCT-AAA (Seq. ID No. 131); TGG-AGC-AAA-TTG-AAG-CCT (Seq. ID No. 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA-E (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG-E (Seq. ID No. 146); TAA-AAA-GAA-AGG-TTC-ATC (Seq. ID No. 147); GCT-TGC-AGA-TAC-TAC-AGA (Seq. ID No. 148); TGA-AAG-CGC-TTA-AAA-CGT (Seq. ID No. 149); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-

TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA (Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 157); TCA-AGG-

CGA-TCG-AAA-TGT (Seq. ID No. 158); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 159); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158); AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159); and

b-) other reagents or compositions necessary to perform the assay.

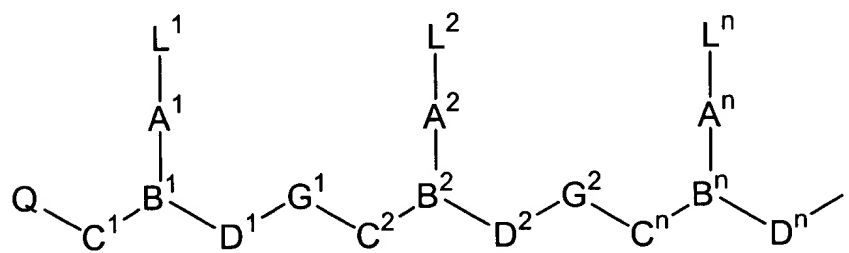
37. (Original) The kit of claim 36, wherein at the probe or probes are unlabeled.
38. (Original) The kit of claim 37, wherein hybridization of the probing nucleobase sequence of the probe to the chromosome is detected using an antibody or antibody fragment, wherein the antibody or antibody fragment specifically binds, under antibody binding conditions, to the PNA/nucleic acid complex which forms under suitable hybridization conditions.
39. (Original) The kit of claim 38, comprising an antibody labeled with a detectable moiety.
40. (Original) The kit of claim 39, wherein the detectable moiety is selected from the group consisting of a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.
41. (Original) The kit of claim 36, wherein at least one non-nucleic acid probe is labeled with a detectable moiety.
42. (Original) The kit of claim 41, wherein the detectable moiety or moieties are selected from the group consisting of: a dextran conjugate, a branched nucleic acid detection system, a chromophore, a fluorophore, a spin label, a radioisotope, an enzyme, a hapten, an acridinium ester and a chemiluminescent compound.

43. (Original) The kit of claim 36, wherein analysis of *in-situ* hybridized specimens is performed using a microscope and camera, a flow cytometer or a slide based analysis system.
44. (Currently Amended) A multiplex assay using ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length to detect, identify or enumerate two or more human chromosomes in the sample, wherein one or more of the ~~non-nucleic acid~~ PNA probes comprise a probing nucleobase sequence, at least a portion of which is, at least ninety percent homologous to the nucleobase sequences, or their complements, selected from the group consisting of: CTT-CAA-AGA-GGT-CCA-CGA (Seq. ID No. 1); AGG-GTT-CAA-CTG-TGT-GAC (Seq. ID No. 2); GAA-ACT-TCT-GAG-TGA-TGA (Seq. ID No. 3); CAG-TCA-TCG-CAG-AAA-ACT (Seq. ID No. 4); AGA-TTT-CAC-TGG-AAA-CGG (Seq. ID No. 5); GTT-ATG-GGA-AGG-TGA-TCC (Seq. ID No. 6); TCG-AGC-CGC-AGA-GTT-TAA (Seq. ID No. 7); CTA-TTT-AGC-GGG-CTT-GGA (Seq. ID No. 8); TAC-AAG-GGT-GTT-GCA-AAC (Seq. ID No. 9); CCA-TAT-GCA-GTT-ATA-AGT-AGG (Seq. ID No. 10); TAT-TGT-ACC-AAG-CAG-AGT-ACC (Seq. ID No. 11); GGT-ATA-TAT-AAG-ATG-ACA-CAG-GA (Seq. ID No. 12); GTT-AGT-TAT-ATT-GGG-TGA-TAT-GT (Seq. ID No. 13); TCA-CAT-AAT-AGA-CAA-CAT-AC (Seq. ID No. 14); CAG-AAG-AGA-TTG-AAC-CTT (Seq. ID No. 15); GGC-ATA-GCA-CAT-AAC-ATG (Seq. ID No. 16); AAT-CGT-CAT-CGA-ATG-AAT (Seq. ID No. 17); CAT-TGA-ACA-GAA-TTG-AAT (Seq. ID No. 18); GTT-TTC-AGG-GGA-AGA-TAT (Seq. ID No. 19); TGT-GCG-CCC-TCA-ACT-AAC (Seq. ID No. 20); GAA-GCT-TCA-TTG-GGA-TGT (Seq. ID No. 21); CCA-ATA-AAA-GCT-ACA-TAG-A (Seq. ID No. 22); GAA-AAA-GTT-TCT-GAC-ATT-GC (Seq. ID No. 23); TAG-TTG-AAG-GGC-ACA-TCA (Seq. ID No. 24); CAC-AAA-TAA-GAT-TCT-AAG-AAT (Seq. ID No. 25); TCA-AAA-GAA-TGC-TTC-AAC-AC (Seq. ID No. 26); ATA-ATT-AGA-CCG-GAA-TCA-T (Seq. ID No. 27); GCT-GTT-TTC-TAA-AGG-AAA-G (Seq. ID No. 28); AAG-ACT-TCA-AAG-AGG-TCC (Seq. ID No. 29); TTT-GTC-AAG-AAT-TAT-AAG-AAG (Seq. ID No. 30); CAA-GAT-TGC-TTT-TAA-TGG (Seq. ID No. 31); TGT-GTA-TCA-ACT-CAC-GGA (Seq. ID No.

32); CCT-CAC-AAA-GTA-GAA-ACT (Seq. ID No. 33); GAA-AAA-GCA-GTT-
 ACT-GAG (Seq. ID No. 34); TAA-TAA-TTA-GAC-GGA-ATC-AT (Seq. ID No.
 35); TTA-CAG-GGC-ATT-GAA-GCC (Seq. ID No. 36); CAG-TTA-TGA-AGC-
 AGT-CTC (Seq. ID No. 37); CAC-ACC-AGA-AAA-AGC-AGT (Seq. ID No. 38);
 AAG-GGT-AAA-CAC-TGT-GAG (Seq. ID No. 39); AGA-CAA-CGA-AAT-ATC-
 TTC-ATG (Seq. ID No. 40); CTA-GCA-GTA-TGA-GGT-CAA (Seq. ID No. 41);
 GCA-GAC-TTC-AGA-AAC-AGA (Seq. ID No. 42); GGC-CTC-AAA-GAC-GTT-
 TAA (Seq. ID No. 43); GTG-AAA-GTT-CCA-AGT-GAA (Seq. ID No. 44); GAG-
 TGC-TTT-GAA-GCC-TAC (Seq. ID No. 45); GAA-ACA-GCA-GAG-TTG-AAA
 (Seq. ID No. 46); TGC-AGA-GAT-CAC-AAC-GTG (Seq. ID No. 47); ACA-AAG-
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 GGC-TTC-AAG-GCG-CTC-TAA (Seq. ID No. 57); GCA-GAG-ACT-TCA-AAG-
 TGC (Seq. ID No. 58); CAC-ACA-CAC-GGT-GGA-CCA (Seq. ID No. 59); CAA-
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 (Seq. ID No. 61); CTC-AAG-GCG-GTC-CAA-TTA (Seq. ID No. 62); GAG-TCG-
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 132); TGG-AGC-ACA-TTT-ATG-CCT (Seq. ID No. 133); TGC-ATT-CTA-CTC-

CCA-TAG (Seq. ID No. 134); ACA-CTC-TGT-TTC-TAA-AAT-CT (Seq. ID No. 135); GCA-GGC-GGA-TAT-TTA-GTA (Seq. ID No. 136); AGC-GAT-TTG-ATG-CCA-ACA (Seq. ID No. 137); TTG-CAA-ACG-GGG-TTT-CTT (Seq. ID No. 138); CTT-TCA-TGC-TAG-ACA-GAA (Seq. ID No. 139); CAA-AAA-AGT-TAC-TGA-GAA-C (Seq. ID No. 140); AAA-ATG-CCA-CAG-CAA-GAG (Seq. ID No. 141); GTT-TGA-AAA-CAC-ACT-GTT-TG (Seq. ID No. 142); ATA-TGG-ACC-TGT-TTG-AGG (Seq. ID No. 143); CAT-TGA-ATG-CTA-GAC-GGA (Seq. ID No. 144); ACG-GGA-TGC-AAT-ATA-AAA (Seq. ID No. 65); TGA-AGA-TTC-TGC-ATA-CGG (Seq. ID No. 66); AAG-GTT-TGT-ACT-GAC-AGA (Seq. ID No. 67); CTG-AAC-TAT-GGT-GAA-AAA (Seq. ID No. 68); ACT-AAC-TGT-GCT-GAA-CAT (Seq. ID No. 69); CCC-ATG-AAT-GCG-AGA-TAG (Seq. ID No. 70); ATG-ATG-AAA-AAG-GTA-ATA-E (Seq. ID No. 145); CAT-TCT-CAG-AAC-TGT-TTG-E (Seq. ID No. 146); AAC-TGA-ACG-CAC-AGA-TGA (Seq. ID No. 71); GGC-TAA-TCT-TTG-AAA-TTG-AAA (Seq. ID No. 72); AGG-TGG-ATA-ATT-GGC-CCT (Seq. ID No. 73); TGA-AGT-CCA-AAA-AAG-CAC (Seq. ID No. 74); CTT-AGA-CAT-GGA-AAT-ATC (Seq. ID No. 75); AAG-GGG-TCT-AAC-TAA-TCA (Seq. ID No. 76); GTA-GTT-GTT-GAG-AAT-GAT (Seq. ID No. 77); AAC-TTC-CCA-GAA-CTA-CAC (Seq. ID No. 78); ATT-CTT-GAA-ATG-GAA-CAC (Seq. ID No. 79); CTG-TGA-TTG-CTG-ATT-TGG (Seq. ID No. 80); GTC-ATC-ACA-GGA-AAC-ATT (Seq. ID No. 81); GAA-ATT-TCC-TGT-TGA-CAG-A (Seq. ID No. 82); GTT-TGA-AAG-CTG-AAC-TAT-G (Seq. ID No. 83); TCC-TGT-AAT-GTT-CGA-CAG (Seq. ID No. 84); TCA-TAG-AAC-GCT-AGA-AAG (Seq. ID No. 85); ACC-TTT-CTT-TTG-ATG-AAG-GA (Seq. ID No. 86); CAA-ATA-TCA-CAA-AAA-GAG-GG (Seq. ID No. 87); GAG-TTG-AAT-AGA-GGC-AAC (Seq. ID No. 88); GGC-CAA-ATG-TAG-AAA-AGG (Seq. ID No. 89); GCG-TTC-AAC-TCA-AGG-TGT (Seq. ID No. 90); TGT-CCT-TTA-GAC-AGA-GCA (Seq. ID No. 91); TGA-GAC-CAA-ATG-TAC-AAA-AG (Seq. ID No. 92); GAA-TAC-TGA-GTA-AGT-TCT-TTG (Seq. ID No. 93); AAC-TGC-ACA-AAT-AGG-GTG (Seq. ID No. 94); TGG-AGA-CAC-TGT-GTT-TGT (Seq. ID No. 95); CCA-GTT-GGA-GAT-TTC-AAT (Seq. ID No. 96); GAA-GCC-TGC-CAG-TGG-ATA (Seq. ID No. 97); TAC-AGC-ATT-CTG-GAA-ACC (Seq. ID No. 98); CCA-GAC-ACT-GCG-TAG-TGA

(Seq. ID No. 99); ATA-TAA-TGC-TAG-AGG-GAG (Seq. ID No. 100); AAA-AAC-AAG-ACA-AAC-TCG (Seq. ID No. 101); ATT-TCA-GCT-GAC-TAA-ACA (Seq. ID No. 102); AAC-GAA-TTA-TGG-TCA-CAT (Seq. ID No. 103); GGT-GAC-GAC-TGA-GTT-TAA (Seq. ID No. 104); TTT-GGA-CCA-CTC-TGT-GGC (Seq. ID No. 105); AAC-GGG-ATA-ACT-GCA-CCT (Seq. ID No. 106); TTT-GTG-GTT-TGT-GGT-GGA (Seq. ID No. 107); AGG-GAA-TAG-CTT-CAT-AGA (Seq. ID No. 108); ATC-ACG-AAG-AAG-GTT-CTG (Seq. ID No. 109); CCG-AAG-ATG-TCT-TTG-GAA (Seq. ID No. 110); AAA-GAG-GTC-TAC-ATG-TCC (Seq. ID No. 111); TTC-CCG-TAA-CAA-CTA-TGC (Seq. ID No. 112); TCC-CGT-AAC-AAC-TAG-GCA (Seq. ID No. 113); AAA-AGG-AGT-GAT-CCA-ACC (Seq. ID No. 114); TCC-CTT-TGG-TAG-AGC-AGG (Seq. ID No. 115); ATT-TGA-GAT-GTG-TGT-ACT-CA (Seq. ID No. 116); GCA-CTT-ACC-GGC-CTA-AG (Seq. ID No. 117); CTC-AGA-AAC-TTA-CTC-GTG (Seq. ID No. 118); ACA-GAA-CTA-AAC-CAT-CGT (Seq. ID No. 147); TAG-GCC-AGC-TTG-GAG-GAT (Seq. ID No. 148); CTA-GCT-GGG-AGG-ATT-T (Seq. ID No. 149); TGT-GCC-TCA-ACT-GAC-A-E (Seq. ID No. 150); TGC-TTT-GGG-ATG-TTT-CAA (Seq. ID No. 151); GCA-ATG-TCA-GAA-CTT-TTT-TC (Seq. ID No. 152); CCG-AAA-GAA-ATT-TGT-GGG (Seq. ID No. 153); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 154); TCA-AGG-CGA-TCG-AAA-TGT (Seq. ID No. 155); GAG-ACA-CAT-ATC-ACC-AAC (Seq. ID No. 156); CAG-AAA-TTT-CTT-TCG-GAT-A (Seq. ID No. 157); GAA-CAT-GGC-CTT-TCA-TAG (Seq. ID No. 158); and AGC-CAA-AGG-AGT-TGA-ACA (Seq. ID No. 159) wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic

moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C¹-Cⁿ is (CR⁶R⁷)_y where R⁶ is hydrogen and R⁷ is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R⁶ and R⁷ are independently selected from the group consisting of hydrogen, (C₂-C₆)alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C₁-C₆)alkoxy, (C₁-C₆)alkylthio, NR³R⁴ and SR⁵, where R³ and R⁴ are as defined above, and R⁵ is hydrogen, (C₁-C₆)alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C₁-C₆)alkyl, or R⁶ and R⁷ taken together complete an alicyclic or heterocyclic system;

each of D¹-Dⁿ is (CR⁶R⁷)_z where R⁶ and R⁷ are as defined above;

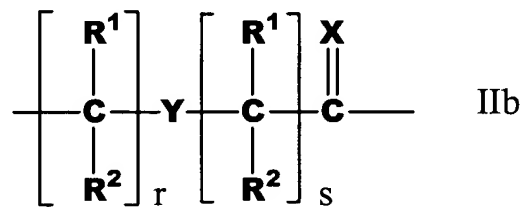
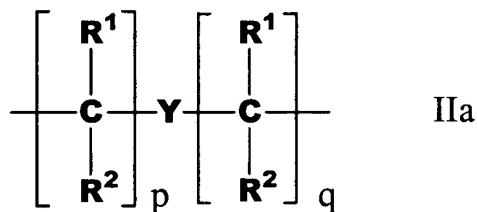
each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

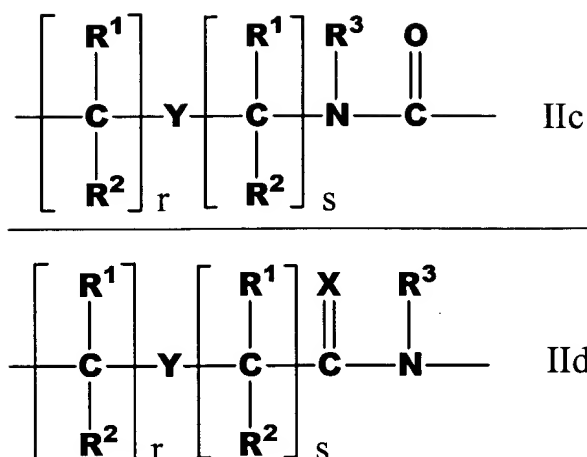
each of G¹-Gⁿ⁻¹ is -NR³CO-, -NR³CS-, -NR³SO- or -NR³SO₂-, in either orientation, where R³ is as defined above;

each of A¹-Aⁿ and B¹-Bⁿ are selected such that:

(a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R³N⁺; or

(b) A is a group of formula (IId) and B is CH₃;





where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

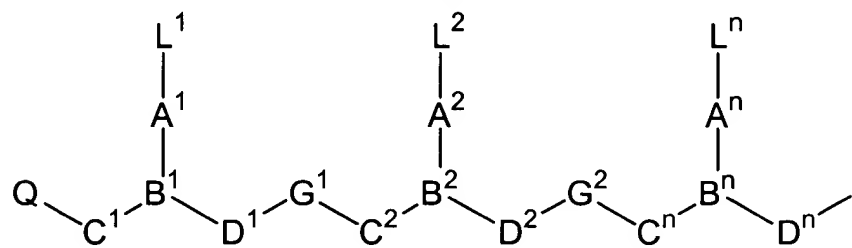
each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is -CO₂H, -CONR'R'', -SO₃H or -SO₂NR'R'' or an activated derivative of -CO₂H or -SO₃H; and

I is -NHR'''R'''' or -NR'''C(O)R''''', where R', R'', R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.

45. (Currently Amended) A prenatal kit for the multiplex analysis of human chromosomes X, Y, 13, 18 and 21, wherein the kit comprises independently

detectable ~~non-nucleic acid~~ PNA probes of 10 to 30 subunits in length for the individual detection of human chromosomes X, Y, 18, as well as human chromosomes 13 and 21 as a pair, and other reagents or components suitable to perform an assay wherein said PNA probe or probes have the formula:



wherein,

n is at least 2,

each of L^1 - L^n is independently selected from the group consisting of hydrogen, hydroxy, (C_1-C_4) alkanoyl, naturally occurring nucleobases, aromatic moieties, DNA intercalators, nucleobase-binding groups, heterocyclic moieties, and reporter ligands;

each of C^1 - C^n is $(CR^6R^7)_y$ where R^6 is hydrogen and R^7 is selected from the group consisting of the side chains of naturally occurring alpha amino acids, or R^6 and R^7 are independently selected from the group consisting of hydrogen, (C_2-C_6) alkyl, aryl, aralkyl, heteroaryl, hydroxy, (C_1-C_6) alkoxy, (C_1-C_6) alkylthio, NR^3R^4 and SR^5 , where R^3 and R^4 are as defined above, and R^5 is hydrogen, (C_1-C_6) alkyl, hydroxy-, alkoxy-, or alkylthio- substituted (C_1-C_6) alkyl, or R^6 and R^7 taken together complete an alicyclic or heterocyclic system;

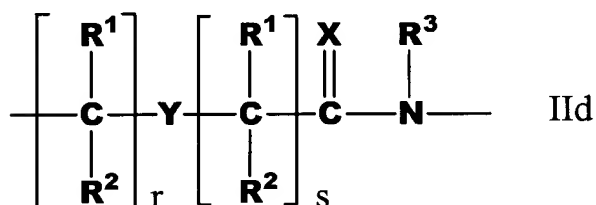
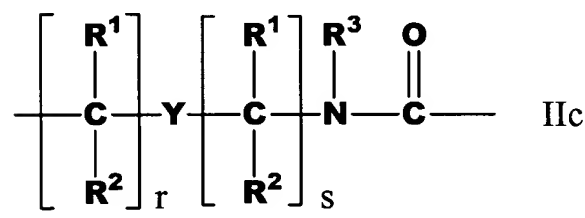
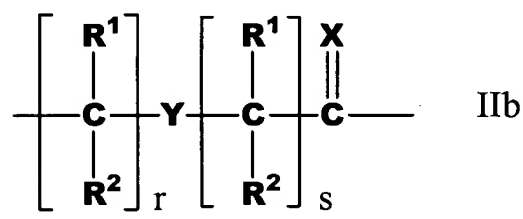
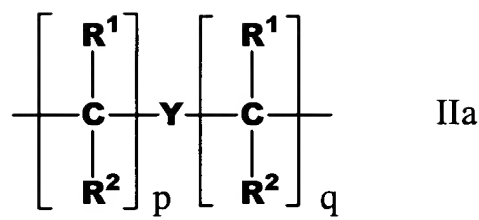
each of D^1 - D^n is $(CR^6R^7)_z$ where R^6 and R^7 are as defined above;

each of y and z is zero or an integer from 1 to 10, the sum y+z being greater than 2 but not more than 10;

each of G^1 - G^{n-1} is $-NR^3CO-$, $-NR^3CS-$, $-NR^3SO-$ or $-NR^3SO_2-$, in either orientation, where R^3 is as defined above;

each of A^1 - A^n and B^1 - B^n are selected such that:

- (a) A is a group of the formula (IIa), (IIb), (IIc), or (IId), and B is N or R^3N^+ ; or
- (b) A is a group of formula (IId) and B is CH;



where:

X is O, S, Se, NR³, CH₂ or C(CH₃)₂;

Y is a single bond, O, S or NR⁴;

each of p and q is zero or an integer from 1 to 5, the sum of p+q being not more than 10;

each of r and s is zero or an integer from 1 to 5, the sum of r+s being not more than 10;

each R¹ and R² is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl which may be hydroxy- or alkoxy- or alkylthio-substituted, hydroxy, alkoxy, alkylthio, amino and halogen; and

each R³ and R⁴ is independently selected from the group consisting of hydrogen, (C₁-C₄)alkyl, hydroxy- or alkoxy- or alkylthio-substituted (C₁-C₄)alkyl, hydroxy, alkoxy, alkylthio and amino;

Q is $-\text{CO}_2\text{H}$, $-\text{CONR}'\text{R}''$, $-\text{SO}_3\text{H}$ or $-\text{SO}_2\text{NR}'\text{R}''$ or an activated derivative of $-\text{CO}_2\text{H}$ or $-\text{SO}_3\text{H}$; and

I is $-\text{NHR}'''\text{R}''''$ or $-\text{NR}'''\text{C}(\text{O})\text{R}''''$, where R' , R'' , R''' and R'''' are independently selected from the group consisting of hydrogen, alkyl, amino protecting groups, reporter ligands, intercalators, chelators, peptides, proteins, carbohydrates, lipids and steroids.